Fig. 9a

Comparative figure of 13K prolamin sequences

```
RM1.(SEQ ID.3)    1:--------------AG--GAAGCATAGTAGTAGAATCCTACAAAAATGAAGATCATTTT
RM4.(SEQ ID.94)   1:--G--CAAA-ATAGAA--AG-ATC-------TAGTGTCCCGCAGCAATGAAGATCATTTT
RM5.(SEQ ID.95)   1:CAATTCAAACATTATAGTTGAAGCATAGTAGTAGAATCCTACAAAAATGAAGATCATTTT
RM7.(SEQ ID.96)   1:--------------GAAGCATAGTAGTAGAATCCAACAACAATGAAGATCATTTT
RM9.(SEQ ID.1)    1:--G--CAAA-AGCATA--AG-AAC-------TAGAAACCCACCACAATGAAGATCATTTT
                              :  : :        :::   ::  :  :::::::::::::::
```

```
RM1.(SEQ ID.3)   61:CGTATTTGCTCTCCTTGCTATTGTTGCATGCAA-CGCTTCTGCACGGTTTGATGCTCTTA
RM4.(SEQ ID.94)  61:CGTCTTTGCTCTCCTTGCTATTGCTGCATGCAG-CGCCTCTGCGCAGTTTGATGTTTTAG
RM5.(SEQ ID.95)  61:CGTATTTGCTCTCCTTGCTATTGTTGCATGCAA-CGCTTCTGCACGGTTTGATGCTCTTA
RM7.(SEQ ID.96)  61:CGTATTTGCTCTCCTTGCTATTGTTGCATGCAATCGC-TCTGCGCGGTTTGATCCTCTTA
RM9.(SEQ ID.1)   61:CTTCTTTGCTCTCCTTGCTATTGCTGCATGCAG-TGCCTCTGCGCAGTTTGATGCTGTTA
                     : : :::::::::::::::::: :::::::::  :: ::::: : ::::::: : :
```

```
RM1.(SEQ ID.3)  121:GTCAAAGTTATAGACAATATCAACTACAATCGCATCTCCTGCTACAGCAACAAGTGCTCA
RM4.(SEQ ID.94) 121:GTCAAAGTTATAGGCAATATCAGCTGCAGTCGCCTGTCCTGCTACAGCAACAGGTGCTTA
RM5.(SEQ ID.95) 121:GTCAAAGTTATAGACAATATCAACTACAATCGCATCTCCTGCTACAGCAACAAGTGCTCA
RM7.(SEQ ID.96) 121:GTCAAAGTTATAGGCAATATCAACTACAGTCGCATCTCCTACTACAGCAACAAGTGCTCA
RM9.(SEQ ID.1)  121:CTCAAGTTTACAGGCAATATCAGCTGCAGCCGCATCTCATGCTGCAGCAACAGATGCTTA
                    :::: ::: :: :::::::: :: ::: : :: : :: : ::::::::::  :::: :
```

```
RM1.(SEQ ID.3)  181:GCCCATGCAGTGAGTTCGTAAGGCAACAGCATAGCATAGTGGCAACCCCCTTCTGGCAAC
RM4.(SEQ ID.94) 181:GCCCATATAATGAGTTCGTAAGGCAGCAGTATGGCATAGCGGCAAGCCCCTTCTTGCAAT
RM5.(SEQ ID.95) 181:GCCCATGCAGTGAGTTCGTAAGGCAACAGCATAGCATAGTGGCAACCCCCTTCTGGCAAC
RM7.(SEQ ID.96) 181:GCCCATGCAGTGAGTTCGTAAGGCAACAGTATAGCATAGTGGCAACCCCCTTCTGGCAAC
RM9.(SEQ ID.1)  181:GCCCATGCGGTGAGTTCGTAAGGCAGCAGTGCAGCACAGTGGCAACCCCCTTCTTCCAAT
                    :::::::  ::::::::::::: :::  ::: ::::: :: : ::  : : : :
```

```
RM1.(SEQ ID.3)  241:CAGCTACGTTTCAATTGATAAACAACCAAGTCATGCAGCAACAGTGTTGCCAACAGCTCA
RM4.(SEQ ID.94) 241:CAGCTGCGTTTCAACTGAGAAACAACCAAGTC-TG--GCAACA--GCT--C-GC-GCT--
RM5.(SEQ ID.95) 241:CAGCTACGTTTCAATTGATAAACAACCAAGTCATGCAGCAACAGTGTTGCCAACAGCTCA
RM7.(SEQ ID.96) 241:CAGCTACGTTTCAATTGATAAACAACCAAGTCATGCAGCAGCAGTGTTGCCAACAGCTCA
RM9.(SEQ ID.1)  241:CACCCGTGTTTCAACTGAGAAACTGCCAAGTCATGCAGCAGCAGTGCTGCCAACAGCTCA
                    :: :  ::::::::  ::: :::: ::::::: ::  ::: ::  :  :  :  : :::
```

Fig. 9b

```
RM1.(SEQ ID.3)   301:GGCTGGTAGCGCAACAATCTCACTACCAGGCCATTAGTAGCGTTCAGGCGATTGTGCAGC
RM4.(SEQ ID.94)  301:GG-TG---GCGCAACAATCTCACTATCAGGACATTAACATTGTTCAGGCCATAGCGCAGC
RM5.(SEQ ID.95)  301:GGCTGGTAGCGCAACAATCTCACTACCAGGCCATTAGTAGCGTTCAGGCGATTGTGCAGC
RM7.(SEQ ID.96)  301:GGCTGGTAGCACAACAATCTCACTACCAGGCCATTAGTATTGTTCAAGCGATTGTGCAAC
RM9.(SEQ ID.1)   301:GGATGATCGCACAACAGTCTCACTGCCAGGCCATTAGCAGTGTTCAGGCTATTGTGCAGC
                       ** **    ** ***** *******  **** *****  *  ***** ** ** * *** *

RM1.(SEQ ID.3)   361:AACTACAGCTGCAGCAGGTCGGTGTT-GTCTACTTTGATCAGACTCAAGCTCAAGCTCAA
RM4.(SEQ ID.94)  361:AGCTACAACTCCAGCAGTTTGGTGATC-TCTACTTTGATCGGAATCTGGCTCAAGCTCAA
RM5.(SEQ ID.95)  361:AACTACAGCTGCAGCAGGTCGGTGTT-GTCTACTTTGATCAGACTCAAGCTCAAGCTCAA
RM7.(SEQ ID.96)  361:AGCTACAACTGCAGCAATTTAGTGGT-GTCTACTTTGATCAGACTCAAGCTCAAGCCCAA
RM9.(SEQ ID.1)   361:AGCTACGGCTACAACAGTTTGCT-AGCGTCTACTTCGATCAGAGTCAAGCTCAAGCCCAA
                       * ****  ** ** **  *   *     ******* **** ** ** *****  *** ***

RM1.(SEQ ID.3)   421:GCTTTGCTGGCCTTAAACTTGCCATCCATATGTGGTATCTATCCTAACTACTACATTGCT
RM4.(SEQ ID.94)  421:GCTCTGTTGGCTTTTAACGTGCCATCTAGATATGGTATCTACCCTAGGTACTATGGTGCA
RM5.(SEQ ID.95)  421:GCTTTGCTGGCCTTAAACTTGCCATCCATATGTGGTATCTATCCTAACTACTACATTGCT
RM7.(SEQ ID.96)  421:ACTCTGTTGACCTTCAACTTGCCATCCATATGTGGTATCTACCCTAACTACTATATGTGCT
RM9.(SEQ ID.1)   421:GCTATGTTGGCCCTAAACATGCCGTCAATATGCGGTATCTACCCAAGCTACAACACTGCT
                       ** ** ** *  * *** ****  ** *  ** ******** ** ** **  * *** *    ***

Rm1.(SEQ ID.3)   481:CCGAGGAGCATTCCCACCGTTGGTGGTGTCTGGTACTGAATTGTAATAGTATAATGGTTC
Rm4.(SEQ ID.94)  481:CCCAGTACCATTACCACCCTTGGCGGTGTCTTGTAATGAGTTTTAACAGTATAGTGGTTC
RM5.(SEQ ID.95)  481:CCGAGGAGCATTCCCACCGTTGGTGGTGTCTGGTACTGAATTGTAACAATATAATAGTTC
RM7.(SEQ ID.96)  481:CCCAGGAGCATTGCCACTGTTGGTGGTGTCTGGTACTGAATTGTAACAATATAATAGTTC
RM9.(SEQ ID.1)   481:CCCTGTAGCATTCCCACCGTCGGTGGTATCTGGTATTGAATTGTAGCAGTATAGTAGTAC
                       **  * * **** ****  * ** ** *** ** *** *** **  * ** * **** * ***

RM1.(SEQ ID.3)   541:AAATGTTAAAAATAAAGTCATGCATCATCATGCGTGAC-AGTTGAAACTTGATGTC-ATA
RM4.(SEQ ID.94)  541:GGAAGTTAAAAATAAGCTCAGATATCAT-ATATGTGACATG-TGAAACTT-TGGGTGATA
RM5.(SEQ ID.95)  541:AAATGTTAAAAATAAAGTCATGCATCATCATGCGTGAC-AGTTGAAA-AAAAAAA--AAA
RM7.(SEQ ID.96)  541:GTATGTTAAAAATAAAGTCATACATCATCATGTGTGAC-TGTTGAAACTTAGGGTC-ATA
RM9.(SEQ ID.1)   541:AGGAGAGAAAAATAAAGTCATGCATCATCATCGTGTGTGACAAGTTGAAACATCGGGGTGATA
                       *  ******** ***  ***** *   ***** * ***** * *****          * *

RM1.(SEQ ID.3)   601:TAAATCTAAAT-AAA-C-TCGTGC-C--------
RM4.(SEQ ID.94)  601:TAAATAGAAAAAAAGTTGTCTTTCATATTTA---
RM5.(SEQ ID.95)  601:AAA-----------------------------
RM7.(SEQ ID.96)  601:TAAATCTAAATAAAATCATCTTAC-CTAAAAAA-
RM9.(SEQ ID.1)   601:CAAATCTGAATAAAAATGTCATGCAAGTTTAAAC
                       **
```
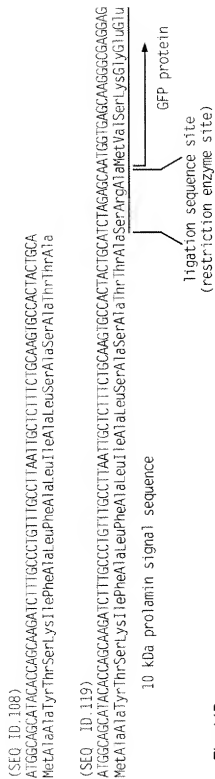
Fig. 14A

(SEQ ID.108)
ATGGCAGCATACACCAGCAAGATCTTTGCCCTGTTTGCCTTAATTGCCTTCTTCGCAAGTGCCACTACTGCA
MetAlaAlaTyrThrSerLysIlePheAlaLeuPheAlaLeuIleAlaLeuSerAlaSerAlaThrThrAla

(SEQ ID.119)
ATGGCAGCATACACCAGCAAGATCTTTGCCCTGTTTGCCTTAATTGCCTTCTTCGCAAGTGCCACTACTGCACCACTACTGCATCTAGAGCAATGGTGAGCAAGGGCGAGGAG
MetAlaAlaTyrThrSerLysIlePheAlaLeuPheAlaLeuIleAlaLeuSerAlaSerAlaThrThrAlaSerArgAlaMetValSerLysGlyGluGlu

10 kDa prolamin signal sequence

ligation sequence site
(restriction enzyme site)

GFP protein

Fig. 14B

original variety

Introducing gene 6 in Fig. 12

(SEQ ID.118)
N-terminal sequence (8 amino acid)
SerArgAlaMetValSerLysGly

13 kDa prolamin